Listing of Claims:

1. (Previously presented) A method for producing DNA, wherein a methylation analysis is used, comprising the steps of:

   a) performing a genome-wide amplification, and

   b) using the amplificates generated in step a) as a standard in the methylation analysis.

2. (Withdrawn) The use of DNA produced by genome-wide amplification methods as a standard in the methylation analysis.

3. (Previously presented) A method of claim 1 wherein the amplification methods performed are PEP, DOP-PCR or linker PCR.

4. (Previously presented) A method of claim 1 wherein the amplification method performed is a multiple displacement amplification (MDA).

5. (Previously presented) A method of claim 4, further comprising using a φ29 polymerase.

6. (Previously presented) A method of claim 4, further comprising using a commercially available kit.

7. (Previously presented) A method of claim 6, wherein the commercially available kits are "GenomiPhi" (Amersham Biosciences) or "Repli-g" (Molecular Staging).

8. (Previously presented) A method of claim 4, further comprising a commercially available DNA produced by MDA is used as a standard.

9. (Previously presented) A method of claim 1 further comprising using restriction

enzymes.

10. (Previously presented) A method of claim 1 further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by methylation-specific ligation methods, MSP, Heavy Methyl or MethyLight.

11. (Previously presented) A method claim 1 further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by primer extension.

12. (Previously presented) A method of claim 1 further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by an amplification and a hybridization of the amplificates at oligomer microarrays.

13. (Previously presented) A method of claim 1 further comprising performing the methylation analysis after conversion of the DNA into a form, in which methylated cytosines can be distinguished from non-methylated cytosines by means of hybridization, by means of a multiplex PCR.

14. (Previously presented) A method of claim 1 wherein a mixture of methylated and non-methylated DNA is used as a standard.

15. (Previously presented) A method of claim 1 wherein several mixtures of methylated and non-methylated DNA with different shares of methylated and non-methylated DNA are used as a standard.

16. (Previously presented) A method of claim 1 wherein the methylation analysis is performed for the diagnosis of cancer diseases or other diseases associated with a modification of the methylation status.

17. (Previously presented) A method of claim 1 wherein the methylation analysis is performed for the prognosis of desired or undesired effects of drugs and for the differentiation of cell types or tissues, or for the investigation of the cell differentiation.

18. (Previously presented) A method for the determination of methylation rates of DNA samples by means of microarrays containing CG and TG oligomers, comprising the steps of:

a) hybridizing the arrays with two calibration standards, which have defined methylation rates;

b) using the hybridization values of step a) to determine a calibration curve for use as a suitable method of calculation; and

c) determining the actual methylation rates of the investigated DNA samples by using this prepared calibration curve.

19. (Previously presented) A method according to claim 18, wherein the two calibration standards have methylation rates of 0% and 100%, respectively.

20. (Previously presented) A method according to claim 18, wherein more than two calibration standards are used, which have different methylation rates.

21. (Previously presented) A method according to claim 18, wherein the actual methylation rates are determined in a multi-stage calculation process, comprising the steps of:

a) normalizing the hybridization values, wherein methylation signals are

determined,

b) normalizing the methylation signals with the aim of variance stabilization, and

c) determining the methylation rates by using the calibration standards and a suitable maximum likelihood algorithm.

22. (Previously presented) A method according to claim 21, further comprising a step prior to step a) wherein the hybridization values are corrected for the background noise inherent in the measurement method.

23. (Withdrawn) A kit comprising reagents for performing a WGA method or DNA amplified already by a WGA method and reagents for performing a bisulphite conversion, and optionally also containing a polymerase, primers and/or probes for an amplification and detection.

24. (Withdrawn) A methylated DNA produced by a WGA method and then methylated by means of an enzyme.

25. (Withdrawn) A methylated DNA produced by a WGA method and then methylated by means of the SssI methylase.

26. (Withdrawn) A mixture of methylated and non-methylated DNA produced by a genome-wide amplification method.

27. (Withdrawn) A mixture of methylated and non-methylated DNA produced by a genome-wide amplification method, wherein the share of methylated DNA is between 5 and 95%.

28. (Withdrawn) A mixture of methylated and non-methylated DNA produced by a

genome-wide amplification method, wherein the share of methylated DNA is between 10 and 80%.

29. (Withdrawn) A mixture of methylated and non-methylated DNA produced by a genome-wide amplification method, wherein the share of methylated DNA is between 25 and 75%.

30. (Withdrawn) The use of the DNA according to claim 24 for the methylation analysis.

31. (Previously presented) A method of claim 1, wherein the genome-wide amplification is performed by exclusively using nucleotides or nucleotide triphosphates, respectively, which are non-methylated.

32. (Withdrawn) A kit comprising reagents for performing a WGA method by exclusively using non-methylated nucleotides or non-methylated nucleotide triphosphates, respectively, or genomic DNA amplified by exclusively using non-methylated nucleotides or non-methylated nucleotide triphosphates, respectively, by WGA method, reagents for performing a bisulphite conversion, and optionally at least one polymerase and primers for an amplification and/or probes for a detection.

33. (Withdrawn) An isolated methylated DNA or mixture of isolated methylated DNA fragments, respectively, obtainable by that genomic DNA is amplified by means of a WGA method by exclusively using non-methylated nucleotides or nucleotide triphosphates, respectively, and the amplified DNA or the mixture of amplified DNA fragments, respectively, is then methylated by means of an enzyme or the SssI methylase.

34. (Withdrawn) A mixture containing methylated and non-methylated DNA, preferably

each from the same organism or from organisms of the same species, wherein the non-methylated DNA was obtained by means of a WGA method by using non-methylated nucleotides or nucleotide triphosphates, respectively, wherein optionally the share of methylated DNA is in the range between 5 and 95 mole-%, in particular between 10 and 80 mole-%, preferably between 25 and 75 mole-%, related to the total content of DNA.

35. (Withdrawn) The use of the DNA according to claim 25 for the methylation analysis.

36. (Withdrawn) The use of the mixture according to claim 26 for the methylation analysis.

37. (Withdrawn) The use of the mixture according to claim 27 for the methylation analysis.

38. (Withdrawn) The use of the mixture according to claim 28 for the methylation analysis.

39. (Withdrawn) The use of the mixture according to claim 29 for the methylation analysis.